

2651224_1.TXT
SEQUENCE LISTINGS

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 <120> CANCER CELL TARGETING GENE DELIVERY METHOD
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 <140> US 10/578,839
 <141> 2006-05-10
 <150> KR 10-2003-0079897
 <151> 2003-11-12
 <150> PCT/KR2004/000545
 <151> 2004-03-15
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 <213> Artificial Sequence
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 <223> 597LN primer
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 <211> 49
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 <213> Artificial Sequence
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 <223> LC597 primer
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<213> Artificial Sequence

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<223> Spike R2 primer

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<211> 36

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<223> LnkNScFv primer

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<213> Artificial Sequence

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<223> ScFvLnkC primer

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<211> 2058

<212> DNA

<213> Gibbon Ape leukemia virus

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<222> (1)..(126)

<220>

<221> misc_feature

<222> (127)..(1467)

<223> surface subunit region

<220>

<221> misc_feature

<222> (1468)..(2025)

<223> transmembrin domain

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atgagtcctg ggagctggaa aagactgac atcctcttaa gctgcgtatt cggcggcggc 120

gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcagggtactg 180

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tggttcaata	actccccctg	gttccactacc	ctgctatcaa	ccatcgctgg	gccctatta	1920
ctcctccttc	tgttgctcat	cctcggggcca	tgcacatca	ataagttagt	tcaattcatc	1980
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<210> 8
 <211> 786
 <212> DNA
 <213> Artificial sequence

<220>
 <223> single-chain antibody Tag-72pS1 specific for Tag-72 surface antigen

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 <221> misc_feature
 <222> (1)..(345)
 <223> heavy chain (H) variable region

<220>
 <221> misc_feature
 <222> (346)..(390)
 <223> (Gly4Ser)3 linker

<220>
 <221> misc_feature
 <222> (391)..(738)
 <223> light chain (L) variable region

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 <221> misc_feature
 <222> (739)..(777)
 <223> PreS1 Tag

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 <221> misc_feature
 <222> (778)..(786)
 <223> C-terminal extra termination sequence

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 cctggacaac gccttgagt gatgggatat ttttctcctg gcaacgatga ttttaaatac 180
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 tacagcagca acaataagaa ctacttagct tggtaccagc agaaaccagg acagcctcct 540
 aagctgctca tttactgggc atctaccgga gaatccgggg tccctgaccg attcagtggc 600
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gtttattact gtcagcaata ttattcctat ccgttgacgt tcggccaagg gaccaagggtg 720
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 <213> Artificial sequence

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<210> 10
 <211> 2871
 <212> DNA
 <213> Artificial Sequence

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 <223> ScFv-GaLV Env GP chimeric peptide (FVGEL199) DNA

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 gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtactg 180
 tcccaaactg gagacgttgt ctgggataca aaggcagtc agcccccttg gacttggtgg 240
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 ggaaccgatg tctcgtcctc taaacgagtc agacctccgg actcagacta tactgccgct 360
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 gcaagctcta ctttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg 480
 tgcggggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt 540
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 ccatgcatca tcaataagtt agttcaattc atcaatgata ggataagtgc agttaaatt 2820
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<210> 11
 <211> 956
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SCFV-GaLV Env GP chimeric ligand (FvGEL199)

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 20 25 30
 Leu Ser Cys Val Phe Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn
 35 40 45
 Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly
 50 55 60
 Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp
 65 70 75 80
 Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser
 85 90 95
 Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Ser Lys Arg Val Arg Pro
 100 105 110
 Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala
 115 120 125
 Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr
 130 135 140
 Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg
 145 150 155 160
 Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr
 165 170 175
 Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr
 180 185 190
 Val Lys Trp Asp Gln Asn Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
 195 200 205
 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
 210 215 220
 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp
 225 230 235 240
 Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Phe Ser
 245 250 255
 Pro Gly Asn Asp Asp Phe Lys Tyr Ser Gln Lys Phe Gln Gly Arg Val
 260 265 270

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Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
 275 280 285
 Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu
 290 295 300
 Asp Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 305 310 315 320
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
 325 330 335
 Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg
 340 345 350
 Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn
 355 360 365
 Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 370 375 380
 Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
 385 390 395 400
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 405 410 415
 Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr
 420 425 430
 Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ala
 435 440 445
 Ala Ala Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro Ala
 450 455 460
 Ala Gly Gly Gly Gly Ser Glu Trp Thr Gln Lys Phe Gln Gln Cys His
 465 470 475 480
 Gln Thr Gly Trp Cys Asn Pro Leu Lys Ile Asp Phe Thr Asp Lys Gly
 485 490 495
 Lys Leu Ser Lys Asp Trp Ile Thr Gly Lys Thr Trp Gly Leu Arg Phe
 500 505 510
 Tyr Val Ser Gly His Pro Gly Val Gln Phe Thr Ile Arg Leu Lys Ile
 515 520 525
 Thr Asn Met Pro Ala Val Ala Val Gly Pro Asp Leu Val Leu Val Glu
 530 535 540
 Gln Gly Pro Pro Arg Thr Ser Leu Ala Leu Pro Pro Pro Leu Pro Pro
 545 550 555 560
 Arg Glu Ala Pro Pro Pro Ser Leu Pro Asp Ser Asn Ser Thr Ala Leu
 565 570 575
 Ala Thr Ser Ala Gln Thr Pro Thr Val Arg Lys Thr Ile Val Thr Leu
 580 585 590
 Asn Thr Pro Pro Pro Thr Thr Gly Asp Arg Leu Phe Asp Leu Val Gln
 595 600 605

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Gly Ala Phe Leu Thr Leu Asn Ala Thr Asn Pro Gly Ala Thr Glu Ser
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 Cys Trp Leu Cys Leu Ala Met Gly Pro Pro Tyr Tyr Glu Ala Ile Ala
 625 630 635 640
 Ser Ser Gly Glu Val Ala Tyr Ser Thr Asp Leu Asp Arg Cys Arg Trp
 645 650 655
 Gly Thr Gln Gly Lys Leu Thr Leu Thr Glu Val Ser Gly His Gly Leu
 660 665 670
 Cys Ile Gly Lys Val Pro Phe Thr His Gln His Leu Cys Asn Gln Thr
 675 680 685
 Leu Ser Ile Asn Ser Ser Gly Asp His Gln Tyr Leu Leu Pro Ser Asn
 690 695 700
 His Ser Trp Trp Ala Cys Ser Thr Gly Leu Thr Pro Cys Leu Ser Thr
 705 710 715 720
 Ser Val Phe Asn Gln Thr Arg Asp Phe Cys Ile Gln Val Gln Leu Ile
 725 730 735
 Pro Arg Ile Tyr Tyr Tyr Pro Glu Glu Val Leu Leu Gln Ala Tyr Asp
 740 745 750
 Asn Ser His Pro Arg Thr Lys Arg Glu Ala Val Ser Leu Thr Leu Ala
 755 760 765
 Val Leu Leu Gly Leu Gly Ile Thr Ala Gly Ile Gly Thr Gly Ser Thr
 770 775 780
 Ala Leu Ile Lys Gly Pro Ile Asp Leu Gln Gln Gly Leu Thr Ser Leu
 785 790 795 800
 Gln Ile Ala Ile Asp Ala Asp Leu Arg Ala Leu Gln Asp Ser Val Ser
 805 810 815
 Lys Leu Glu Asp Ser Leu Thr Ser Leu Ser Glu Val Val Leu Gln Asn
 820 825 830
 Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys Glu Gly Gly Leu Cys Ala
 835 840 845
 Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ile Asp His Ser Gly Ala Val
 850 855 860
 Arg Asp Ser Met Lys Lys Leu Lys Glu Lys Leu Asp Lys Arg Gln Leu
 865 870 875 880
 Glu Arg Gln Lys Ser Gln Asn Trp Tyr Glu Gly Trp Phe Asn Asn Ser
 885 890 895
 Pro Trp Phe Thr Thr Leu Leu Ser Thr Ile Ala Gly Pro Leu Leu Leu
 900 905 910
 Leu Leu Leu Leu Leu Ile Leu Gly Pro Cys Ile Ile Asn Lys Leu Val
 915 920 925
 Gln Phe Ile Asn Asp Arg Ile Ser Ala Val Lys Ile Leu Val Leu Arg
 930 935 940

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Gln Lys Tyr Gln Ala Leu Glu Asn Glu Gly Asn Leu
945 950 955